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Molecular tracing of viral haemorrhagic septicaemia viruses from Denmark provides evidence of more viral clades and cases of introduction through long distance transportation

Søren Kahns, Helle Frank Skall, Søren Peter Jonstrup, Katja Einer-Jensen, David Stone, and Niels Jørgen Olesen

Viral haemorrhagic septicaemia (VHS) is a serious rhabdoviral disease that infects rainbow trout. The disease may cause up to 80% mortality and is listed by the OIE as a notifiable disease. Based on the full length glycoprotein gene (G-gene) sequences previous studies have identified 4 robust genotypes of the virus, designated I - IV with a geographic basis for their distribution. Genotype I have been further divided into five sub-types designated Ia – Ie of which the fresh water VHSV genotype Ia is responsible for the majority of losses in rainbow trout aquaculture in Europe. Denmark has been considered to be endemically infected by VHSV until 2009 where the country obviously has freed itself from the disease through a VHS eradication program. To study evolutionary dynamics of VHSV genotype Ia isolates in Danish aquaculture, the G-gene from all isolates causing outbreaks in Danish rainbow trout farms since 2004 have been sequenced. Phylogenetic analyses including these sequences and several isolates from outbreaks in other European countries showed that genotype Ia isolates can be further divided into a number of different clades of which one comprise Danish strains and another comprises strains from central European outbreaks. Coupling of phylogenetic and geographical information data was used to trace origins of virus populations and the spreading of the disease. Both spreading due to contact infection through water and by movement of fish was observed. The outcome from this study will constitute an important background for optimizing the design and strategies for prevention and surveillance of VHS.